(c) determining the relative hybridization of the probes to the target nucleic acid,

(d) estimating the sequence of the target nucleic acid from the relative hybridization of the probes;

(e) providing a further array of probes comprising a probe set comprising probes complementary to the estimated sequence of the target nucleic acid;

(f) hybridizing the target nucleic acid to the further array of probes;

(g) determining the relative hybridization of the probes to the target nucleic acid;

(h) reestimating the sequence of the target nucleic acid from the relative hybridization of the probes.

2. (amended) The method of claim 1, further comprising repeating steps (e)-(h) as necessary until the reestimated sequence of the target nucleic acid is [the true sequence of the target nucleic acid] constant between successive cycles.

3. The method of claim 1, wherein the target nucleic acid is a species variant of the reference sequence.

4. The method of claim 1, wherein the reference sequence is from a human and the target nucleic acid is from a primate.

5. The method of claim 1, wherein the target nucleic acid shows 50-99% sequence identity with the reference sequence.

6. The method of claim 1, wherein the target nucleic acid shows 80-95% sequence identity with the reference sequence.

7. The method of claim 1, wherein the reference sequence is at least 1000 nucleotides long, the array comprises a probe set comprising overlapping probes that are perfectly complementary to and span the reference sequence, and the further array comprises probes that are perfectly complementary to and span the estimated sequence.

8. (Amended) The method of claim 1, wherein an estimated sequence of the target nucleic acid includes [a position of ambiguity] a nucleotide whose identity is ambiguous and the probe set showing perfect complementarity to the estimated sequence includes a probe having[including] a pooled nucleotide aligned with the position of ambiguity in the target sequence.

9. The method of claim 1, wherein the reference sequence is at least 10 kb.

10. The method of claim 1, wherein the reference sequence is at least 1000 kb.

11. The method of claim 1, wherein the reference sequence includes at least 90% of the human genome.

12. The method of claim 1, wherein the array of probes comprises:

(1)   a first probe set comprising a plurality of probes, each probe comprising a segment of at least six nucleotides exactly complementary to a subsequence of the reference sequence, the segment including at least one interrogation position complementary to a corresponding nucleotide in the reference sequence,

(2) second, third and fourth probe sets, each comprising a corresponding probe for each probe in the first probe set, the probes in the second, third and fourth probe sets being identical to a sequence comprising the corresponding probe from the first probe set or a subsequence of at least six nucleotides thereof that includes the at least one interrogation position, except that the at least one interrogation position is occupied by a different nucleotide in each of the four corresponding probes from the four probe sets.

13. The method of claim 12, wherein the sequence of the target nucleic acid is estimated by:

(a)   comparing the relative specific binding of four corresponding probes from the first, second, third and fourth probe sets;

(b)   assigning a nucleotide in the sequence of the target nucleic acid as the complement of the interrogation position of the probe having the greatest specific binding;

(c)   repeating (a) and (b) until each nucleotide of interest in the sequence of the target nucleic acid has been estimated.

14. The method of claim 1, wherein the sequence of the target nucleic acid differs from the reference by at least two positions within a probe length.

15. A method of analyzing a target nucleic acid, comprising:

(a) designing an array of probes to be complementary to an estimated sequence of the target nucleic acid,

(b) hybridizing the array of probes to the target nucleic acid;

(c) determining a reestimated sequence of the target nucleic acid from the hybridization pattern of the array to the target nucleic acid sequence to; and

(d) repeating (a)-(c) at least once.

Remarks

Support for the amendment to claim 1 is provided at e.g., p. 7, line 12-14 (designing an array to a known reference sequence) and at p. 8, lines 12-13 (target sequence a variant of a reference sequence). Support for the amendment to claim 2 is provided at p. 7, line 25, and for the amendment to claim 8 at the paragraph bridging pp. 11-12. The amendments are for purposes of clarity and should not be construed as an acquiescence in any ground of rejection. The Examiner's specific comments are now addressed using the paragraph numbering of the office action.

1-2. The Examiner says it is not clear what is meant by a "true" sequence and how it was measured. The claim has been amended to recite that the reestimated sequence remains constant between successive iterations (thereby indicating convergence toward the true sequence).

The Examiner says reference to a "position of ambiguity" is unclear in claim 8, as is the inclusion of both "having" and "including." The claim has been amended to clarify that the ambiguity resides in the identity of a nucleotide. The term "including" has been deleted.

3-4. Claims 1-2 and 5-15 stand rejected as anticipated by Cronin. The Examiner takes the view that Cronin discloses each of the eight steps (a)-(h) recite in claim 1. For steps (e)-(h) which recite the second iteration of the presently claimed method, the